

Sequences producing significant alignments:	Score (bits)	E Value
gi 21739860 emb CAD38956.1 hypothetical protein [Homo sapiens]	502	e-140
gi 21903449 sp O95157 NXP3_HUMAN Neurexophilin 3 precursor ...	501	e-140
gi 27754212 ref NP_009156.1 neurexophilin 3 [Homo sapiens]...	498	e-139
gi 18699994 ref NP_570928.1 neurexophilin 3 [Mus musculus]...	493	e-138
gi 11067403 ref NP_067711.1 neurexophilin 3 [Rattus norvegicus]...	491	e-137
gi 6330146 dbj BAA86473.1 KIAA1159 protein [Homo sapiens]	435	e-120
gi 4105166 qb AAD02281.1 neurexophilin 3 [Homo sapiens]	335	2e-90
gi 23097338 ref NP_689958.1 neurexophilin 1 [Homo sapiens]...	252	2e-65
gi 26339006 dbj BAC33174.1 unnamed protein product [Mus musculus]...	252	2e-65
gi 6981298 ref NP_037126.1 neurexophilin 1 [Rattus norvegicus]...	252	2e-65
gi 2498667 sp Q61200 NXP1_MOUSE Neurexophilin 1 precursor >...	252	2e-65
gi 21750075 dbj BAC03713.1 unnamed protein product [Homo sapiens]...	250	9e-65
gi 45598386 ref NP_032777.2 neurexophilin 1 [Mus musculus]...	250	9e-65
gi 10720136 sp O95156 NXP2_HUMAN Neurexophilin 2 precursor ...	244	5e-63
gi 42656449 ref XP_371573.2 neurexophilin 2 [Homo sapiens]	244	5e-63
gi 47212189 emb CAF95222.1 unnamed protein product [Tetraodon lineatus]...	244	5e-63
gi 27806033 ref NP_776831.1 neurexophilin 2 [Bos taurus] >...	244	5e-63
gi 42600548 dbj BAD11132.1 neurexophilin2 [Homo sapiens]	244	5e-63
gi 47218764 emb CAG02750.1 unnamed protein product [Tetraodon lineatus]...	243	1e-62
gi 47215019 emb CAG01843.1 unnamed protein product [Tetraodon lineatus]...	241	3e-62

gi 34853244 ref XP_231055.2	similar to Neurexophilin 2 pre...	239	1e-61	L
gi 33468865 ref NP_032778.1	neurexophilin 2 [Mus musculus]...	237	6e-61	L
gi 2498670 sp Q61199 NXP2 MOUSE	Neurexophilin 2 precursor >...	235	3e-60	L
gi 21759327 sp Q8WMJ4 NXP3 MACMU	Neurexophilin 3 >gi 174838...	196	2e-48	
gi 21759326 sp Q8WMI6 NXP1 MACMU	Neurexophilin 1 >gi 174839...	155	3e-36	
gi 47220448 emb CAG03228.1	unnamed protein product [Tetrao...	127	1e-29	
gi 47219722 emb CAG12644.1	unnamed protein product [Tetrao...	126	2e-27	
gi 39930315 ref NP_009155.1	neurexophilin 4 [Homo sapiens]...	113	2e-23	L
gi 11067405 ref NP_067712.1	neurexophilin 4 [Rattus norveg...	113	2e-23	L
gi 4105168 gb AAD02282.1	neurexophilin 4 [Homo sapiens]	112	3e-23	L
gi 30581034 sp O95158 NXP4 HUMAN	Neurexophilin 4 precursor ...	110	1e-22	L
gi 21759328 sp Q8WMJ7 NXP4 MACMU	Neurexophilin 4 >gi 174838...	104	6e-21	
gi 34304109 ref NP_899120.1	neurexophilin 4 [Mus musculus]...	100	9e-20	L
gi 38080930 ref XP_358860.1	similar to hypothetical protei...	47	0.001	L
gi 34868030 ref XP_221539.2	similar to hypothetical protei...	47	0.001	L
gi 21450781 ref NP_659474.1	hypothetical protein MGC15606 ...	47	0.002	L
gi 32822864 gb AAH55004.1	Unknown (protein for MGC:57066) ...	44	0.010	
gi 47226931 emb CAG05823.1	unnamed protein product [Tetrao...	41	0.081	
gi 46119362 ref ZP_00176475.2	COG1716: FOG: FHA domain [Cr...	40	0.24	
gi 22538453 ref NP_683721.1	phosphatidylinositol glycan, c...	39	0.40	L
gi 47228791 emb CAG07523.1	unnamed protein product [Tetrao...	39	0.40	
gi 22135346 gb AAM93156.1	Glisl Kruppel-like zinc finger p...	39	0.53	L
gi 46445001 gb EAL04272.1	hypothetical protein CaO19.13345...	38	0.69	
gi 15840405 ref NP_335442.1	PE_PGRS family protein [Mycoba...	38	0.90	
gi 40744228 gb EAA63404.1	hypothetical protein AN2833.2 [A...	38	0.90	
gi 39595465 emb CAE60503.1	Hypothetical protein CBG04122 [...	37	1.2	
gi 47213943 emb CAF94474.1	unnamed protein product [Tetrao...	37	1.5	
gi 38100429 gb EAA47559.1	hypothetical protein MG02802.4 [...	37	1.5	
gi 34527710 dbj BAC85439.1	unnamed protein product [Homo s...	28	1.6	
gi 39645603 gb AAH63705.1	Unknown (protein for MGC:75563) ...	28	1.8	
gi 38105516 gb EAA51935.1	hypothetical protein MG03530.4 [...	37	2.0	
gi 47221651 emb CAF97916.1	unnamed protein product [Tetrao...	36	2.6	
gi 41615498 tpg DAA03507.1	TPA: HDC00764 [Drosophila melan...	36	2.6	
gi 995557 emb CAA61623.1	DRPLA [Rattus norvegicus]	36	2.6	
gi 8393274 ref NP_058924.1	dentatorubral pallidoluysian at...	36	2.6	L
gi 46390822 dbj BAD16327.1	hypothetical protein [Oryza sat...	36	3.4	
gi 34871343 ref XP_221996.2	similar to hypothetical protei...	36	3.4	L
gi 31792170 ref NP_854663.1	PE-PGRS FAMILY PROTEIN [Mycoba...	36	3.4	
gi 15608120 ref NP_215495.1	PE_PGRS [Mycobacterium tubercu...	36	3.4	
gi 34856045 ref XP_214950.2	similar to RIKEN cDNA 2610034E...	36	3.4	L
gi 46390090 dbj BAD15507.1	hypothetical protein [Oryza sat...	36	3.4	
gi 38104079 gb EAA50700.1	hypothetical protein MG04459.4 [...	36	3.4	
gi 46193155 ref ZP_00207576.1	COG4664: TRAP-type mannitol/...	35	4.4	
gi 27370418 ref NP_766509.1	hypothetical protein C130036J1...	35	4.4	L
gi 33438588 ref NP_872301.1	hypothetical protein FLJ25224 ...	35	4.4	L
gi 37718972 ref NP_937803.1	RIKEN cDNA 5930405J04 [Mus mus...	35	4.4	L
gi 39580550 emb CAE74682.1	Hypothetical protein CBG22492 [...	35	4.4	
gi 31791933 ref NP_854426.1	PE-PGRS FAMILY PROTEIN [Mycoba...	35	4.4	
gi 31207243 ref XP_312588.1	ENSANGP00000014942 [Anopheles ...	35	4.4	
gi 21741306 emb CAD41269.1	OSJNBb0103I08.8 [Oryza sativa (...	35	4.4	
gi 34535174 dbj BAC87231.1	unnamed protein product [Homo s...	35	4.4	L
gi 15840160 ref NP_335197.1	PE_PGRS family protein [Mycoba...	35	4.4	
gi 37182729 gb AAQ89165.1	brush border [Homo sapiens]	35	4.4	L

gi 15607887 ref NP_215261.1	PE_PGRS [Mycobacterium tubercu...	35	4.4	
gi 32409235 ref XP_325098.1	predicted protein [Neurospora ...	35	4.4	
gi 48095523 ref XP_397525.1	hypothetical protein XP_397525...	35	4.4	L
gi 1168094 gb AAB35238.1	IRS-2, 4PS=insulin and cytokine s...	35	5.8	
gi 38109508 gb EAA55367.1	hypothetical protein MG09174.4 [...	35	5.8	
gi 34904556 ref NP_913625.1	B1066G12.23 [Oryza sativa (jap...	35	5.8	
gi 5305335 gb AAD41594.1	proline-rich mucin homolog [Mycob...	35	5.8	
gi 39586345 emb CAE74002.1	Hypothetical protein CBG21638 [...	35	7.6	
gi 37530618 ref NP_919611.1	unknown protein [Oryza sativa ...	35	7.6	
gi 9758692 dbj BAB09308.1	unnamed protein product [Arabido...	35	7.6	
gi 7330072 gb AAF60061.1	ORFRU4-R [Macaca mulatta rhadinov...	35	7.6	
gi 42734353 ref NP_080414.1	RIKEN cDNA 6330407J23 [Mus mus...	35	7.6	L
gi 34328110 ref NP_031907.2	dentatorubral pallidoluysian a...	35	7.6	L
gi 1549217 dbj BAA13450.1	DRPLA protein [Mus musculus]	35	7.6	L
gi 4520376 dbj BAA75913.1	uridylyl transferase [Pseudomona...	35	7.6	
gi 39933290 ref NP_945566.1	possible OmpA family member [R...	35	7.6	
gi 2842529 dbj BAA24679.1	otx/orthodenticle related homeop...	35	7.6	
gi 22972987 ref ZP_00019835.1	hypothetical protein [Chloro...	35	7.6	
gi 15842929 ref NP_337966.1	hypothetical protein [Mycobact...	34	9.9	
gi 16944521 emb CAB97476.2	conserved hypothetical protein ...	34	9.9	
gi 22299354 ref NP_682601.1	phosphoribosyl formylglycinami...	34	9.9	
gi 29828953 ref NP_823587.1	hypothetical protein SAV2411 [...	34	9.9	
gi 15341763 gb AAH13045.1	SWI/SNF-related matrix-associate...	34	9.9	L
gi 21237808 ref NP_620706.1	SWI/SNF-related matrix-associa...	34	9.9	L
gi 33147038 dbj BAC80121.1	hypothetical protein [Oryza sat...	34	9.9	
gi 30583979 gb AAP36238.1	Homo sapiens SWI/SNF related, ma...	34	9.9	
gi 32405440 ref XP_323333.1	predicted protein [Neurospora ...	34	9.9	

Alignments

Get selected sequences

Select all

Deselect all

☐ >gi|21739860|emb|CAD38956.1| **L** hypothetical protein [Homo sapiens]
Length = 372

Score = 502 bits (1292), Expect = e-140
Identities = 242/269 (89%), Positives = 242/269 (89%)
Frame = +1

Query: 1 LGPXXXXXXXXXXXXXXXXXQLTRCCFVFLVQGSLLYLVICGQDDGPPGSEDPERDDHEGQP 180
LGP MQLTRCCFVFLVQGSLLYLVICGQDDGPPGSEDPERDDHEGQP
Sbjct: 103 LGPRKEKGRARGRERRRRKQLTRCCFVFLVQGSLLYLVICGQDDGPPGSEDPERDDHEGQP 162

Query: 181 RPRVPRKRGHISPKSRPMANSTLLGLLAPPGEAWGILGQXXXXXXXXXXXXAKVKKIFGW 360
RPRVPRKRGHISPKSRPMANSTLLGLLAPPGEAWGILGQ AKVKKIFGW
Sbjct: 163 RPRVPRKRGHISPKSRPMANSTLLGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFGW 222

Query: 361 GDFYSNIKTVALNLLVTGKIVDHGNGTFSVHFQHNATGQGNISISLVPPSKAVEFHQEQQ 540
GDFYSNIKTVALNLLVTGKIVDHGNGTFSVHFQHNATGQGNISISLVPPSKAVEFHQEQQ
Sbjct: 223 GDFYSNIKTVALNLLVTGKIVDHGNGTFSVHFQHNATGQGNISISLVPPSKAVEFHQEQQ 282

Query: 541 IFIEAKASKIFNCRMEWEKVERGRRTSLCTHDPAKICSRDHAQSSATWSCSQPFKVVCVY 720
IFIEAKASKIFNCRMEWEKVERGRRTSLCTHDPAKICSRDHAQSSATWSCSQPFKVVCVY
Sbjct: 283 IFIEAKASKIFNCRMEWEKVERGRRTSLCTHDPAKICSRDHAQSSATWSCSQPFKVVCVY 342

Query: 721 IAFYSTDYRLVQKVC PDYNYHSDTPYYPS 807
IAFYSTDYRLVQKVC PDYNYHSDTPYYPS
Sbjct: 343 IAFYSTDYRLVQKVC PDYNYHSDTPYYPS 371

☐ >gi|21903449|sp|O95157|NXP3_HUMAN ☒ Neurexophilin 3 precursor (UNQ687/PRO1327)
gi|37182175|gb|AAQ88890.1| ☒ NXP3 [Homo sapiens]
Length = 252

Score = 501 bits (1289), Expect = e-140
Identities = 239/251 (95%), Positives = 239/251 (95%)
Frame = +1

Query: 55 MQLTRCCFVFLVQGS LYLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPM 234
MQLTRCCFVFLVQGS LYLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPM
Sbjct: 1 MQLTRCCFVFLVQGS LYLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPM 60

Query: 235 ANSTLLGLLAPPGEAWGILGQXXXXXXXXXXXXAKVKKIFGWGDFYSNIKTVALNLLVTG 414
ANSTLLGLLAPPGEAWGILGQ AKVKKIFGWGDFYSNIKTVALNLLVTG
Sbjct: 61 ANSTLLGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFGWGDFYSNIKTVALNLLVTG 120

Query: 415 KIVDHGNGTFSVHFQHNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMWE 594
KIVDHGNGTFSVHFQHNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMWE
Sbjct: 121 KIVDHGNGTFSVHFQHNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMWE 180

Query: 595 KVERGRRTSLCTHDPAKICSRDHAQSSATWSCSQPFKVVVCVYIAFYSTDYRLVQKVC PDY 774
KVERGRRTSLCTHDPAKICSRDHAQSSATWSCSQPFKVVVCVYIAFYSTDYRLVQKVC PDY
Sbjct: 181 KVERGRRTSLCTHDPAKICSRDHAQSSATWSCSQPFKVVVCVYIAFYSTDYRLVQKVC PDY 240

Query: 775 NYHSDTPYYPS 807
NYHSDTPYYPS
Sbjct: 241 NYHSDTPYYPS 251

☐ >gi|27754212|ref|NP_009156.1| ☒ neurexophilin 3 [Homo sapiens]
gi|18490705|gb|AAH22541.1| ☒ Neurexophilin 3 [Homo sapiens]
Length = 252

Score = 498 bits (1282), Expect = e-139
Identities = 238/251 (94%), Positives = 238/251 (94%)
Frame = +1

Query: 55 MQLTRCCFVFLVQGS LYLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPM 234
MQLTRCCFVFLVQGS LYLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPM
Sbjct: 1 MQLTRCCFVFLVQGS LYLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPM 60

Query: 235 ANSTLLGLLAPPGEAWGILGQXXXXXXXXXXXXAKVKKIFGWGDFYSNIKTVALNLLVTG 414
ANSTLLGLLAPPGEAWGILGQ AKVKKIFGWGDFYSNIKTVALNLLVTG
Sbjct: 61 ANSTLLGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFGWGDFYSNIKTVALNLLVTG 120

Query: 415 KIVDHGNGTFSVHFQHNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMWE 594
KIVDHGNGTFSVHFQHNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRM WE
Sbjct: 121 KIVDHGNGTFSVHFQHNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMWE 180

Query: 595 KVERGRRTSLCTHDPAKICSRDHAQSSATWSCSQPFKVVVCVYIAFYSTDYRLVQKVC PDY 774
KVERGRRTSLCTHDPAKICSRDHAQSSATWSCSQPFKVVVCVYIAFYSTDYRLVQKVC PDY

Sbjct: 181 KVERGRRTSLCTHDPKICSRDHAQSSATWSCSQPFKVVVCVYIAFYSTDYRLVQKVC PDY 240

Query: 775 NYHSDTPYYPS 807

NYHSDTPYYPS

Sbjct: 241 NYHSDTPYYPS 251

☐ >gi|18699994|ref|NP_570928.1| ☒ L neurexophilin 3 [Mus musculus]
 gi|21759329|sp|Q91VX5|NXP3_MOUSE ☒ L Neurexophilin 3 precursor
 gi|13938105|gb|AAH07167.1| ☒ L Neurexophilin 3 [Mus musculus]
 gi|26332927|dbj|BAC30181.1| ☒ L unnamed protein product [Mus musculus]
 Length = 252

Score = 493 bits (1269), Expect = e-138
 Identities = 233/251 (92%), Positives = 236/251 (94%)
 Frame = +1

Query: 55 MQLTRCCFVFLVQGSlyLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPM 234
 MQLTRCCFVFLVQGSlyLVICGQDDGPPGSEDPE DDHEGQPRPRVPRKRGHISPKSRP+
 Sbjct: 1 MQLTRCCFVFLVQGSlyLVICGQDDGPPGSEDPEHDDHEGQPRPRVPRKRGHISPKSRPL 60

Query: 235 ANSTLLGLLAPPGEAWGILGQXXXXXXXXXXXXAKVKKIFGWGDFYSNIKTVALNLLVTG 414
 ANSTLLGLLAPPGE WG+LGQ KVKKIFGWGDFYSNIKTVALNLLVTG
 Sbjct: 61 ANSTLLGLLAPPGEVWGVLGQPPNRPKQSPPLSTKVKKIFGWGDFYSNIKTVALNLLVTG 120

Query: 415 KIVDHGNGTFSVHFQHNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMewe 594
 KIVDHGNGTFSVHF+HNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMewe
 Sbjct: 121 KIVDHGNGTFSVHFHRNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMewe 180

Query: 595 KVERGRRTSLCTHDPKICSRDHAQSSATWSCSQPFKVVVCVYIAFYSTDYRLVQKVC PDY 774
 KVERGRRTSLCTHDPKICSRDHAQSSATWSCSQPFKVVVCVYIAFYSTDYRLVQKVC PDY
 Sbjct: 181 KVERGRRTSLCTHDPKICSRDHAQSSATWSCSQPFKVVVCVYIAFYSTDYRLVQKVC PDY 240

Query: 775 NYHSDTPYYPS 807

NYHSDTPYYPS

Sbjct: 241 NYHSDTPYYPS 251

☐ >gi|11067403|ref|NP_067711.1| ☒ L neurexophilin 3 [Rattus norvegicus]
 gi|10720140|sp|Q9Z2N5|NXP3_RAT Neurexophilin 3 precursor
 gi|4104961|gb|AAD02226.1| ☒ L neurexophilin 3 [Rattus norvegicus]
 Length = 252

Score = 491 bits (1265), Expect = e-137
 Identities = 232/251 (92%), Positives = 236/251 (94%)
 Frame = +1

Query: 55 MQLTRCCFVFLVQGSlyLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPM 234
 MQLTRCCFVFLVQGSlyLVICGQ+DGPPGSEDPE DDHEGQPRPRVPRKRGHISPKSRP+
 Sbjct: 1 MQLTRCCFVFLVQGSlyLVICGQEDGPPGSEDPEHDDHEGQPRPRVPRKRGHISPKSRPL 60

Query: 235 ANSTLLGLLAPPGEAWGILGQXXXXXXXXXXXXAKVKKIFGWGDFYSNIKTVALNLLVTG 414
 ANSTLLGLLAPPGE WGILGQ KVKKIFGWGDFYSNIKTVALNLLVTG
 Sbjct: 61 ANSTLLGLLAPPGEVWGILGQPPNRPKQSPPLSTKVKKIFGWGDFYSNIKTVALNLLVTG 120

Query: 415 KIVDHGNGTFSVHFQHNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMewe 594

KIVDHGNGTFSVHF+HNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMWEWE
 Sbjct: 121 KIVDHGNGTFSVHFRHNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMWEWE 180
 Query: 595 KVERGRRTSLCTHDPAKICSRDHAQSSATWSCSQPFKVVCVYIAFYSTDYRLVQKVCPCDY 774
 KVERGRRTSLCTHDPAKICSRDHAQSSATWSCSQPFK+VCVYIAFYSTDYRLVQKVCPCDY
 Sbjct: 181 KVERGRRTSLCTHDPAKICSRDHAQSSATWSCSQPFKIVCVYIAFYSTDYRLVQKVCPCDY 240
 Query: 775 NYHSDTPYYPS 807
 NYHSDTPYYPS
 Sbjct: 241 NYHSDTPYYPS 251

☐ >gi|6330146|dbj|BAA86473.1| ☒ KIAA1159 protein [Homo sapiens]
 Length = 221

Score = 435 bits (1118), Expect = e-120
 Identities = 208/220 (94%), Positives = 208/220 (94%)
 Frame = +1

Query: 148 DPERDDHEGQPRPRVPRKRGHISPKSRPMANSTLLGLLAPPGEAWGILGQXXXXXXXXXXXX 327
 DPERDDHEGQPRPRVPRKRGHISPKSRPMANSTLLGLLAPPGEAWGILGQ
 Sbjct: 1 DPERDDHEGQPRPRVPRKRGHISPKSRPMANSTLLGLLAPPGEAWGILGQPPNRPNHSP 60
 Query: 328 XXAKVKKIFGWGDFYSNIKTVALNLLVTGKIVDHGNGTFSVHFQHNATGQGNISISLVPP 507
 AKVKKIFGWGDFYSNIKTVALNLLVTGKIVDHGNGTFSVHFQHNATGQGNISISLVPP
 Sbjct: 61 PSAKVKKIFGWGDFYSNIKTVALNLLVTGKIVDHGNGTFSVHFQHNATGQGNISISLVPP 120
 Query: 508 SKAVEFHQEQQIFIEAKASKIFNCRMWEWEKVERGRRTSLCTHDPAKICSRDHAQSSATWS 687
 SKAVEFHQEQQIFIEAKASKIFNCRMWEWEKVERGRRTSLCTHDPAKICSRDHAQSSATWS
 Sbjct: 121 SKAVEFHQEQQIFIEAKASKIFNCRMWEWEKVERGRRTSLCTHDPAKICSRDHAQSSATWS 180
 Query: 688 CSQPFKVVCVYIAFYSTDYRLVQKVCPCDYNHSDTPYYPS 807
 CSQPFKVVCVYIAFYSTDYRLVQKVCPCDYNHSDTPYYPS
 Sbjct: 181 CSQPFKVVCVYIAFYSTDYRLVQKVCPCDYNHSDTPYYPS 220

☐ >gi|4105166|gb|AAD02281.1| ☒ neurexophilin 3 [Homo sapiens]
 Length = 173

Score = 335 bits (860), Expect = 2e-90
 Identities = 158/158 (100%), Positives = 158/158 (100%)
 Frame = +1

Query: 334 AKVKKIFGWGDFYSNIKTVALNLLVTGKIVDHGNGTFSVHFQHNATGQGNISISLVPPSK 513
 AKVKKIFGWGDFYSNIKTVALNLLVTGKIVDHGNGTFSVHFQHNATGQGNISISLVPPSK
 Sbjct: 15 AKVKKIFGWGDFYSNIKTVALNLLVTGKIVDHGNGTFSVHFQHNATGQGNISISLVPPSK 74
 Query: 514 AVEFHQEQQIFIEAKASKIFNCRMWEWEKVERGRRTSLCTHDPAKICSRDHAQSSATWSCS 693
 AVEFHQEQQIFIEAKASKIFNCRMWEWEKVERGRRTSLCTHDPAKICSRDHAQSSATWSCS
 Sbjct: 75 AVEFHQEQQIFIEAKASKIFNCRMWEWEKVERGRRTSLCTHDPAKICSRDHAQSSATWSCS 134
 Query: 694 QPFKVVCVYIAFYSTDYRLVQKVCPCDYNHSDTPYYPS 807
 QPFKVVCVYIAFYSTDYRLVQKVCPCDYNHSDTPYYPS
 Sbjct: 135 QPFKVVCVYIAFYSTDYRLVQKVCPCDYNHSDTPYYPS 172

☐ >gi|23097338|ref|NP_689958.1| ☒ L neurexophilin 1 [Homo sapiens]
 gi|17433155|sp|P58417|NXP1_HUMAN ☒ L Neurexophilin 1 precursor
 gi|15823301|dbj|BAB69044.1| ☒ L neurexophilin 1 [Homo sapiens]
 gi|28703720|gb|AAH47505.1| ☒ L Neurexophilin 1 [Homo sapiens]
 Length = 271

Score = 252 bits (643), Expect = 2e-65
 Identities = 109/157 (69%), Positives = 136/157 (86%)
 Frame = +1

Query: 337 KVKKIFGWGDFYSNIKTVALNLLVTGKIVDHGNGTFSVHFQHNATGQGNISISLVPPSKA 516
 K KK+FGWGDF+SNIKTV LNLL+TGKIVDHGNGTFSV+F+HN+TGQGN+S+SLVPP+K
 Sbjct: 114 KFKKMFGWGDFHSNIKTVALNLLITGKIVDHGNGTFSVYFRHNSTGQGNVSVSLVPPTKI 173
 Query: 517 VEFHQEQQIFIEAKASKIFNCRMEWEKVERGRRTSLCTHDPAKICSRDHAQSSATWSCSQ 696
 VEF QQ I+AK SK FNCR+E+EKV++ + +LC +DP+K C ++ QS +W CS+
 Sbjct: 174 VEFDLAQQTVIDAKDSKSFNCRIEYKVDKATKNTLCNYDPSKTCYQEQTQSHVSWLCSK 233
 Query: 697 PFKVVCVYIAFYSTDYRLVQKVC PDYNYHSDTPYYPS 807
 PFKV+C+YI+FYSTDY+LVQKVC PDYNYHSDTPY+PS
 Sbjct: 234 PFKVICIYISFYSTDYKLVQKVC PDYNYHSDTPYFPS 270

☐ >gi|26339006|dbj|BAC33174.1| ☒ L unnamed protein product [Mus musculus]
 gi|26350181|dbj|BAC38730.1| ☒ L unnamed protein product [Mus musculus]
 Length = 271

Score = 252 bits (643), Expect = 2e-65
 Identities = 109/157 (69%), Positives = 136/157 (86%)
 Frame = +1

Query: 337 KVKKIFGWGDFYSNIKTVALNLLVTGKIVDHGNGTFSVHFQHNATGQGNISISLVPPSKA 516
 K KK+FGWGDF+SNIKTV LNLL+TGKIVDHGNGTFSV+F+HN+TGQGN+S+SLVPP+K
 Sbjct: 114 KFKKMFGWGDFHSNIKTVALNLLITGKIVDHGNGTFSVYFRHNSTGQGNVSVSLVPPTKI 173
 Query: 517 VEFHQEQQIFIEAKASKIFNCRMEWEKVERGRRTSLCTHDPAKICSRDHAQSSATWSCSQ 696
 VEF QQ I+AK SK FNCR+E+EKV++ + +LC +DP+K C ++ QS +W CS+
 Sbjct: 174 VEFDLAQQTVIDAKDSKSFNCRIEYKVDKATKNTLCNYDPSKTCYQEQTQSHVSWLCSK 233
 Query: 697 PFKVVCVYIAFYSTDYRLVQKVC PDYNYHSDTPYYPS 807
 PFKV+C+YI+FYSTDY+LVQKVC PDYNYHSDTPY+PS
 Sbjct: 234 PFKVICIYISFYSTDYKLVQKVC PDYNYHSDTPYFPS 270

☐ >gi|6981298|ref|NP_037126.1| ☒ L neurexophilin 1 [Rattus norvegicus]
 gi|2498668|sp|Q63366|NXP1_RAT ☒ L Neurexophilin 1 precursor (Neurophilin)
 gi|508574|gb|AAB18420.1| ☒ L neurexophilin [Rattus norvegicus]
 Length = 271

Score = 252 bits (643), Expect = 2e-65
 Identities = 109/157 (69%), Positives = 136/157 (86%)
 Frame = +1

Query: 337 KVKKIFGWGDFYSNIKTVALNLLVTGKIVDHGNGTFSVHFQHNATGQGNISISLVPPSKA 516
 K KK+FGWGDF+SNIKTV LNLL+TGKIVDHGNGTFSV+F+HN+TGQGN+S+SLVPP+K

Sbjct: 114 KFKKMFGWGDFHSNIKTVKLNLLITGKIVDHGNGTFSVYFRHNSTGQGNVSVSLVPPTKI 173

Query: 517 VEFHQEQQIFIEAKASKIFNCRMWEKVERGRRTSLCTHDPAKICSRDHAQSSATWSCSQ 696
 VEF QQ I+AK SK FNCR+E+EKV++ + +LC +DP+K C ++ QS +W CS+

Sbjct: 174 VEFDLAQQTVIDAKDSKSFNCRIEYKVDKATKNTLCNYDPSKTCYQEQTQSHVSWLCSK 233

Query: 697 PFKVVCVYIAFYSTDYRLVQKVC PDYNYHSDTPYYPS 807
 PFKV+C+YI+FYSTDY+LVQKVC PDYNYHSDTPY+PS

Sbjct: 234 PFKVICIYISFYSTDYKLVQKVC PDYNYHSDTPYFPS 270

☐ >gi|2498667|sp|Q61200|NXP1_MOUSE ☒ Neurexophilin 1 precursor
 gi|1336015|gb|AAB18764.1| ☒ neurexophilin 1 [Mus musculus]
 Length = 253

Score = 252 bits (643), Expect = 2e-65
 Identities = 109/157 (69%), Positives = 136/157 (86%)
 Frame = +1

Query: 337 KVKKIFGWGDFYSNIKTVALNLLVTGKIVDHGNGTFSVHFQHNATGQGNISISLVPPSKA 516
 K KK+FGWGDF+SNIKTV LNLL+TGKIVDHGNGTFSV+F+HN+TGQGN+S+SLVPP+K

Sbjct: 96 KFKKMFGWGDFHSNIKTVKLNLLITGKIVDHGNGTFSVYFRHNSTGQGNVSVSLVPPTKI 155

Query: 517 VEFHQEQQIFIEAKASKIFNCRMWEKVERGRRTSLCTHDPAKICSRDHAQSSATWSCSQ 696
 VEF QQ I+AK SK FNCR+E+EKV++ + +LC +DP+K C ++ QS +W CS+

Sbjct: 156 VEFDLAQQTVIDAKDSKSFNCRIEYKVDKATKNTLCNYDPSKTCYQEQTQSHVSWLCSK 215

Query: 697 PFKVVCVYIAFYSTDYRLVQKVC PDYNYHSDTPYYPS 807
 PFKV+C+YI+FYSTDY+LVQKVC PDYNYHSDTPY+PS

Sbjct: 216 PFKVICIYISFYSTDYKLVQKVC PDYNYHSDTPYFPS 252

☐ >gi|21750075|dbj|BAC03713.1| ☒ unnamed protein product [Homo sapiens]
 Length = 271

Score = 250 bits (638), Expect = 9e-65
 Identities = 108/157 (68%), Positives = 136/157 (86%)
 Frame = +1

Query: 337 KVKKIFGWGDFYSNIKTVALNLLVTGKIVDHGNGTFSVHFQHNATGQGNISISLVPPSKA 516
 K KK+FGWGDF+SNIKTV LNLL+TGKIVDHG+GTFSV+F+HN+TGQGN+S+SLVPP+K

Sbjct: 114 KFKKMFGWGDFHSNIKTVKLNLLITGKIVDHGSGTFSVYFRHNSTGQGNVSVSLVPPTKI 173

Query: 517 VEFHQEQQIFIEAKASKIFNCRMWEKVERGRRTSLCTHDPAKICSRDHAQSSATWSCSQ 696
 VEF QQ I+AK SK FNCR+E+EKV++ + +LC +DP+K C ++ QS +W CS+

Sbjct: 174 VEFDLAQQTVIDAKDSKSFNCRIEYKVDKATKNTLCNYDPSKTCYQEQTQSHVSWLCSK 233

Query: 697 PFKVVCVYIAFYSTDYRLVQKVC PDYNYHSDTPYYPS 807
 PFKV+C+YI+FYSTDY+LVQKVC PDYNYHSDTPY+PS

Sbjct: 234 PFKVICIYISFYSTDYKLVQKVC PDYNYHSDTPYFPS 270




☐ >gi|45598386|ref|NP_032777.2| ☒ neurexophilin 1 [Mus musculus]
 gi|26336020|dbj|BAC31708.1| ☒ unnamed protein product [Mus musculus]
 Length = 271

Score = 250 bits (638), Expect = 9e-65
 Identities = 108/157 (68%), Positives = 135/157 (85%)
 Frame = +1

Query: 337 KVKKIFGWGDFYSNIKTVALNLLVTGKIVDHGNGTFSVHFQHNATGQGNISISLVPPSKA 516
 K KK+FGWGDF+SNIKTV LNLL+TGKIVDHGNG FSV+F+HN+TGQGN+S+SLVPP+K
 Sbjct: 114 KFKKMFGWGDFHSNIKTVKLNLLITGKIVDHGNGNFSVYFRHNSTGQGNVSVSLVPPTKI 173

Query: 517 VEFHQEQQIFIEAKASKIFNCRMEWEKVERGRRTSLCTHDPKICSRDHAQSSATWSCSQ 696
 VEF QQ I+AK SK FNCR+E+EKV++ + +LC +DP+K C ++ QS +W CS+
 Sbjct: 174 VEFDLAQQTVIDAKDSKSFNCRIEYKVDKATKNTLCNYDPSKTCYQEQTQSHVSWLCSK 233

Query: 697 PFKVVCVYIAFYSTDYRLVQKVC PDYNYHSDTPYYPS 807
 PFKV+C+YI+FYSTDY+LVQKVC PDYNYHSDTPY+PS
 Sbjct: 234 PFKVICIYISFYSTDYKLVQKVC PDYNYHSDTPYFPS 270

 >gi|10720136|sp|O95156|NXP2_HUMAN  Neurexophilin 2 precursor
 gi|4105164|gb|AAD02280.1|  neurexophilin 2 [Homo sapiens]
 Length = 262

Score = 244 bits (623), Expect = 5e-63
 Identities = 107/157 (68%), Positives = 131/157 (83%)
 Frame = +1

Query: 337 KVKKIFGWGDFYSNIKTVALNLLVTGKIVDHGNGTFSVHFQHNATGQGNISISLVPPSKA 516
 K KK+FGWGDF+SNIKTV LNLL+TGKIVDHGNGTFSV+F+HN+TG GN+S+SLVPPSK
 Sbjct: 105 KFKKMFGWGDFHSNIKTVKLNLLITGKIVDHGNGTFSVYFRHNSTGLGNVSVSLVPPSKV 164

Query: 517 VEFHQEQQIFIEAKASKIFNCRMEWEKVERGRRTSLCTHDPKICSRDHAQSSATWSCSQ 696
 VEF Q +E K SK FNCR+E+EK +R ++T+LC DP+KIC ++ QS +W CS+
 Sbjct: 165 VEFVSPQSTLETESKSFNCRIEYKTDRAKKTALCNFDPSKICYQEQTQSHVSWLCSK 224

Query: 697 PFKVVCVYIAFYSTDYRLVQKVC PDYNYHSDTPYYPS 807
 PFKV+C+YIAFY S DY+LVQKVC PDYNYHS+TPY S
 Sbjct: 225 PFKVICIYIAFYSDYKLVQKVC PDYNYHSETPYLSS 261

 >gi|42656449|ref|XP_371573.2|  neurexophilin 2 [Homo sapiens]
 Length = 347

Score = 244 bits (623), Expect = 5e-63
 Identities = 107/157 (68%), Positives = 131/157 (83%)
 Frame = +1

Query: 337 KVKKIFGWGDFYSNIKTVALNLLVTGKIVDHGNGTFSVHFQHNATGQGNISISLVPPSKA 516
 K KK+FGWGDF+SNIKTV LNLL+TGKIVDHGNGTFSV+F+HN+TG GN+S+SLVPPSK
 Sbjct: 190 KFKKMFGWGDFHSNIKTVKLNLLITGKIVDHGNGTFSVYFRHNSTGLGNVSVSLVPPSKV 249

Query: 517 VEFHQEQQIFIEAKASKIFNCRMEWEKVERGRRTSLCTHDPKICSRDHAQSSATWSCSQ 696
 VEF Q +E K SK FNCR+E+EK +R ++T+LC DP+KIC ++ QS +W CS+
 Sbjct: 250 VEFVSPQSTLETESKSFNCRIEYKTDRAKKTALCNFDPSKICYQEQTQSHVSWLCSK 309

Query: 697 PFKVVCVYIAFYSTDYRLVQKVC PDYNYHSDTPYYPS 807
 PFKV+C+YIAFY S DY+LVQKVC PDYNYHS+TPY S
 Sbjct: 310 PFKVICIYIAFYSDYKLVQKVC PDYNYHSETPYLSS 346